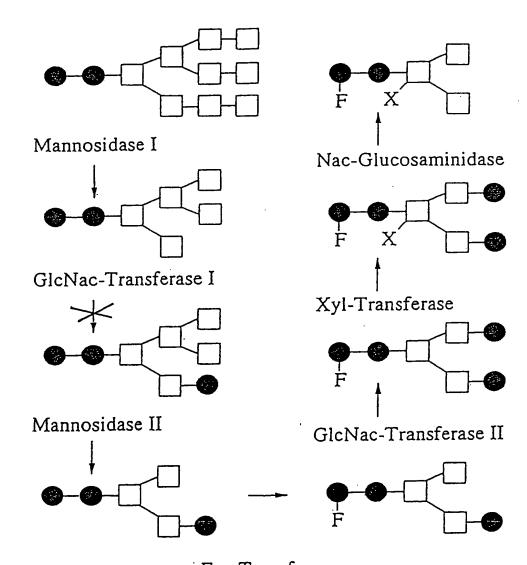
TITLE: PLANT GNTI SEQUENCES AND THE USE THEREOF FOR THE PRODUCTION OF PLANTS HAVING REDUCED OR LACKING N-ACETYL GLUCOSAMINYL TRANSFERASE I(GNTI) ACTIVITY INVENTOR(S): ANTJE VON SCHAEWEN

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Figure 1



Fuc-Transferase

TITLE: PLANT GNTI SEQUENCES AND THE USE THEREOF FOR THE PRODUCTION OF PLANTS HAVING REDUCED OR LACKING N-ACETYL GLUCOSAMINYL TRANSFERASE I(GNTI) ACTIVITY

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Figure 2 Al GntI cDNA

GAAT"	TCG(cea (CCGC	CTGA(GA A	ACCC'	rcga	A TT	CAAT	ITCG	CAT	rtgg(CAG	AG A'	rG et 1	55
AGA (GGG Gly	AAC Asn	AAG Lys 5	TTT Phe	CÀ2 ICC	TTT Phe	GAT Asp	TTA Leu 10	CGG Arg	TAC Tyr	CTT Leu	CTC Leu	GTC Val 15	GTG Val	GCT Ala	103
GCT (CTC Leu	GCC Ala 20	TTC Phe	ATC Ile	TAC Tyr	ATA Ile	CAG <i>Gln</i> 25	ATG Met	CGG Arg	CTT Leu	TTC Phe	GCG Ala 30	ACA Thr	CAG Gln	TCA Ser	. 151
GAA 1 Glu 1	TAT Tyr 35	GTA Val	GAC Asp	CGC Arg	CTT Leu	GCT Ala 40	GCT Ala	GCA Ala	ATT Ile	GAA Glu	GCA Ala 45	GAA Glu	AAT Asn	CAT His	TGT Cys	199
ACA I	AGT Ser	CAG Gln	ACC Thr	AGA Arg	TTG Leu 55	CTT Leu	ATT Ile	GAC Asp	AAG Lys	ATT Ile 60	AGC Ser	CAG Gln	CAG Gln	CAA Gln	GGA Gly 65	247
AGA (GTA Val	GTA Val	GCT Ala	CTT Leu 70	GAA Glu	GAA Glu	CAA Gln	ATG Met	AAG Lys 75	CAT His	CAG Gln	GAC Asp	CAG Gln	GAG Glu 80	TGC Cys	295
CGG (CAA Gln	TTA Leu	AGG Arg 85	GCT Ala	CTT Leu	GTT Val	CAG Gln	GAT Asp 90	CTT Leu	GAA Glu	AGT Ser	AAG Lys	GGC Gly 95	ATA Ile	AAA Lys	343
AAG 1 Lys I	TTA Leu	ATC Ile 100	GGA Gly	GAT Asp	GTG Val	CAG Gln	ATG Met 105	CCA Pro	GTG. Val	GCA Ala	GCT Ala	GTA Val 110	GTT Val	GTT Val	ATG Met	391
GCT 1	TGC Cys 115	AGT Ser	CGT Arg	ACT Thr	GAC Asp	TAC Tyr 120	CTG Leu	GAG Glu	AGG Arg	ACT Thr	ATT Ile 125	AAA Lys	TCC Ser	ATC Ile	TTA Leu	439
AAA 1 Lys 1 130	TAC Tyr	CAA Gln	ACA Thr	TCT Ser	GTT Val 135	GCA Ala	TCA Ser	AAA Lys	TAT Tyr	CCT Pro 140	CTT Leu	TTC Phe	ATA Ile	TCC	CAG Gln 145	487
GAT (GGA Gly	TCA Ser	AAT Asn	CCT Pro 150	GAT Asp	GTA Val	AGA Arg	AAG Lys	CTT Leu 155	GCT Ala	TTG Leu	AGC Ser	TAT Tyr	GGT Gly 160	CAG Gln	535
CTG A	ACG Thr	ŤAT Tyr	ATG Met 165	CAG Gln	CAC His	TTG Leu	GAT Asp	TAT Tyr 170	GAA Glu	CCT Pro	CTG Val	CAT His	ACT Thr 175	GAA Glu	AGA Arg	583
CCA C	GGG Gly	GAA Glu 180	CTG Leu	GTT Val	GCA Ala	TAC Tyr	TAC Tyr 185	AAG Lys	ATT Ile	GCA Ala	CGT Arg	CAT His 190	TAC Tyr	AAG Lys	TGG Trp	631
GCA TALA	TTG Leu 195	GAT Asp	CAG Gln	CTG Leu	TTT -Phe	CAC His 200	AAG Lys	CAT His	AAT Asn	TTT Phe	AGC Ser 205	CGT Arg	GTT Val	ATC Ile	ATA Ile	679
CTA C Leu C 210	GAA Glu	GAT Asp	GAT Asp	ATG Met	GAA Glu 215	ATT Ile	GCT Ala	GCT Ala	GAT Asp	TTT Phe 220	TTT Phe	GAC Asp	TAT Tyr	TTT Phe	GAG Glu 225	727

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Figure 2 (continued)

GCT GGA GCT ACT CTT GAC AGA GAC AAG TCG ATT ATG GCT ATT TCT Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile Ser. 230 235 240	775					
TCT TGG AAT GAC AAT GGA CAA AGG CAG TTC GTC CAA GAT CCT GAT GCT Ser Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp Ala 245 250 255	823					
CTT TAC CGC TCA GAC TTT TTT CCT GGT CTT GGA TGG ATG CTT TCA AAA Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser Lys 260 265 270	871					
TCA ACT TGG TCC GAA CTA TCT CCA AAG TGG CCA AAG GCT TAC TGG GAT Ser Thr Trp Ser Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp 275 280 285	919					
GAC TGG CTA AGG CTG AAA GAA AAT CAC AGA GGT CGA CAA TTT ATT CGC Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile Arg 290 295 300 305	967					
CCA GAA GTT TGC AGA ACG TAC AAT TTT GGT GAG CAT GGT TCT AGT TTG Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu 310 315 320	1015					
GGG CAG TTT TTT AAG CAG TAT CTT GAG CCA ATT AAG CTA AAT GAT GTC Gly Gln Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val 325 330 335	1063					
CAG GTT GAT TGG AAG TCA ATG GAC CTA AGT TAC CTT TTG GAG GAC AAC Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp Asn 340 345 350	1111					
TAT GTG AAA CAC TTT GGC GAC TTG GTT AAA AAG GCT AAG CCC ATC CAC Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile His 355 360 365	1159					
GGA GCT GAT GCT GTT TTG AAA GCA TTT AAC ATA GAT GGT GAT GTG CGT Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val Arg 370 385	1207					
ATT CAG TAC AGA GAC CAA CTA GAC TTT GAA GAT ATC GCT CGA CAG TTT Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln Phe 390 395 400	1255					
GGC ATT TTT GAA GAA TGG AAG GAT GGT GTA CCA CGG GCA GCA TAT AAA Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr Lys 405 410 415	1303					
GGG ATA GTA GTT TTC CGG TTT CAA ACA TCT AGA CGT GTG TTC CTT GTT Gly Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu Val 420 425 430	1351					
TCC CCT GAT TCT CTT CGA CAA CTT GGA GTT GAA GAT ACT TAG Ser Pro Asp Ser Leu Arg Gln Leu Gly Val Glu Asp Thr End 435 440 445	1393					
CGAAGATATG ATTGGAGCCT GAGCAACAAT TTAGACTTAT TTGGTAGGAT ACATTTGAAA	1453					
GAGCTGACAC GAAAAGTATG ACTACCAGTA GCTACATGCA ACATTTTAAT GTTAATGGAA	1513					
GGAACCCACT GCTTATTGTT GGAATGGATG AATCATCACC ACATCCTATT ATTCAAGTTT 1						
ACAAACATAA AGAGGAAATG TTGCCCTATA AAAACAAATT TTTTGTTTCT AAGAAGGAAC	1633					
GTTACGATTA TGAGCAACTT TGGCGGCCGC GAATTC	1669					

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Figure 3A

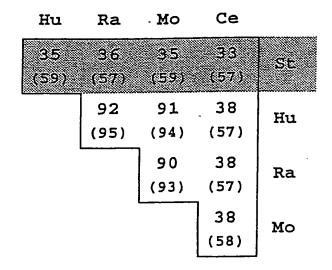


Figure 3B

A_Stb-A1	1	MRGNKFCFDLRYLL AA AFIYIOMRLFATOSEYVDRLAAAIEAENHCT
B_Ntb-A9	1	MRGNKFCCDFRYLLI AA AFIYFOMRLFATOSEYADRLAAAIEAENHCT
C_Atb-Full	1	MAFISCDLRELLIFAAFMFIYIOMRLFOTOSEYADRLSAAIESENHCT
A_Stb-Al	51	SOTRLLIDKISOOOGREVALEEOMKEODOECROLRALVODLESKGIKKLI
B_Ntb-A9	51	SOTRLLIDGISGOOGRIVALEEOMKRODOECROLRALVODLESKGIKKLI
C_Atb-Full	49	SOMRGLIDGISGOSRIVALEEMKNRODEELVOLKOLGOTEEKKGIAKLT
A_Stb-Al	101	GMVQMPVAAVVVMACSRMDYLERTIKSILKYQTSVASKYPLFISQDGSMP
B_Ntb-A9	101	GMVQMPVAAVVVMACNRADYLEMTIKSILKYQTSVASKYPLFISQDGSMP
C_Atb-Full	99	QGGQMPVAAVVVMACSRADYLERTÄKSMLMYQTPVASKYPLFISQDGSMQ
A_Stb-Al	151	DVRKLALSYGOLTYMOHLD EPVHTERPGEL AYYKIARHYKWALDOLFH
B_Ntb-A9	151	DVRKLALSYGOLTYMOHLDFEPVHTERPGEL AYYKIARHYKWALDOLFY
C_Atb-Full	149	AVESKSLSYMOLTYMOHLDFEPVVTERPGEL AYYKIARHYKWALDOLFY
A_Stb-Al	201	KHNFSRVIILEDDMEIAMDFFDYFEAGATLLDRDKSIMAISSWNDNGOMO
B_Ntb-A9	201	KHNFSRVIILEDDMEIAPDFFDMFEAGATLLDRDKSIMAISSWNDNGOMO
C_Atb-Full	199	KHMFSRVIILEDDMEIAPDFFDYFEAMASLMDRDKMIMAMSSWNDNGOMO
A_Stb-Al	251	EVODPDALYRSDFFPGLGWMLSKSTWSELSPKWPKAYWDDWLRLKENHRG
B_Ntb-A9	251	EVODPYALYRSDFFPGLGWMLSKSTWDELSPKWPKAYWDDWLRLKENHRG
C_Atb-Full	249	FVEDPYALYRSDFFPGLGWMLKESTWDELSPKWPKAYWDDWLRLKENHEG
A_stb-Al	301	ROFIRPEVCRTYNFGEHGSSLGOFFKOYLEPIKLNDVOVDWKSMDLSYLL
B_ntb-A9	301	ROFIRPEVCRTYNFGEHGSSLGOFFKOYLEPIKLNDVOVDWKSMDLSYLL
C_Atb-Full	299	ROFIMPEVCRTYNFGEHGSSLGOFFSOYLEPIKLNDVTVDWKKKDLGYLT
A_Stb-Al	351	EDNYVKHEGDLVKKAKPIHGADAVLKAFNIDGDVRIQYRDQLDFEMIARQ
B_Ntb-A9.	351	EDNYVKHEGDLVKKAKPIHGADAVLKAFNIDGDVRIQYRDQLDFEMIARQ
C_Atb-Full	349	EGNY <mark>TKYESG</mark> LVFQAFPIQGEDLVLKAQNIKDDDRIRYEDQFFERIA <mark>G</mark> P
A_Stb-Al	401	FGIFEEWKDGVPRAAYKGIVVFREQTSRRVFLVSPDSLRQLGEEDT
B_Ntb-A9	401	FGIFEEWKDGVPRAAYKGIVVFREQTSRRVFLVGEDSLQQLGIEDT
C_Atb-Full	399	FGIFEEWKDGVPREAYKGEVVFREQTERRVFLVGPDSEMQLGIRES

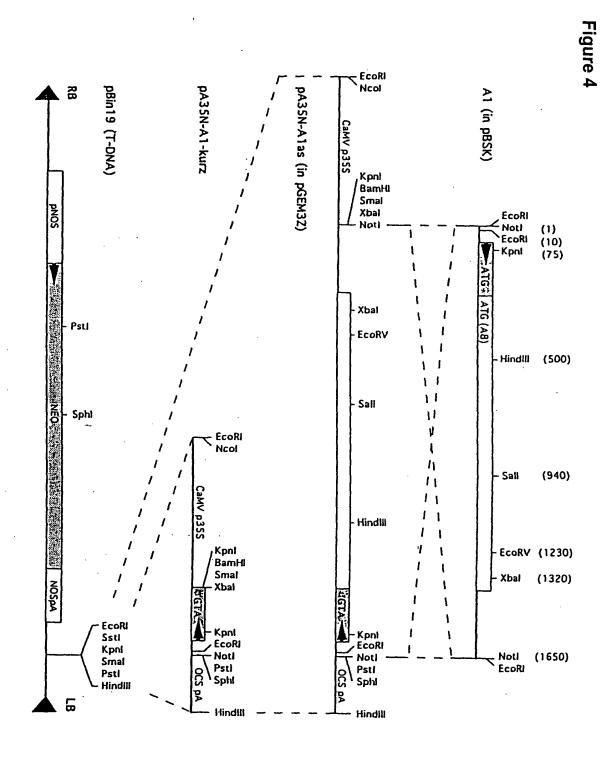
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INVENTOR(S): ANTJE VON SCHAEWEN ATTORNEY DOCKET NO. 032266-004

Figure 5

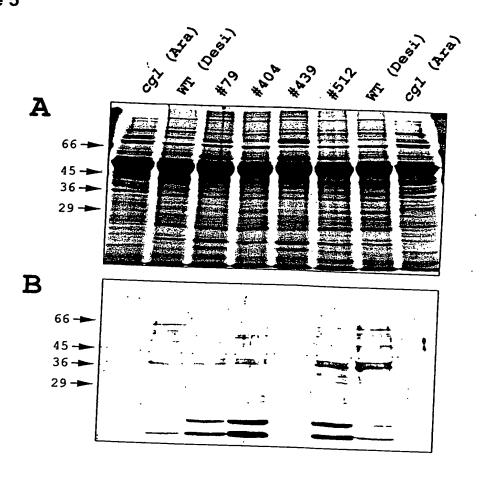


Figure 6

